


```
/function="add ADP-ribose"
/codon_start=1
/product="poly(ADP)-ribose polymerase"
/protein_id="AAC79704.1"
/db_xref="GI:3928871"
/translation="MAAPKAWAEYAKSGRASCSCRSPIAKDQLRLCKMVAQSQFD
GPMPMNHARCFISKKNQIKSDVDDGIDALRWDDQEKIRNIVGVSASAGTSSIAAPPE
KFTIEIAPARTSCRRCSSEKIKGVSRLSAKLESEKPGKIPWTHANCFFEVSPSATVE
KFSQWDTLSDKRTMLDLVKDVGNEQNKSKRSKSENDIDSYKASRLDESTSEGT
VRNGQLVDPGRSNTSSADIQKLKEQSDTLWKLDGLKTHVSAALRDLMLANGODT
SGPERHLIDRCADGMLFGALGPCVANGMYVNGOCNGVSEWSEKTYGATEPVR
VRRKQIPHTGKNDYLMKFKSKOKYKPERVLPMSPEKSGSKATORTSILSSKGLDK
LRRSVQCSKEAANEWLEKLAGANFYARVADKIDICLACGELDENENAEVKARELK
IPIVREGYIGECVKKNNKMLPFYDLKLENALESSKSTVTYVKKGRSAVHESGLQDTA
HILEDGKSIYNATLNNMSDLALGVNSYVLIQIIEODDGSCEYVFKRWGRVSEKIGQK
LEEMSKTEAIKEFKRLFLKFTGNSWEAWECKTNFRKQPGRFYPLDYDYGKKAPKRD
ISEMSSIALPOLLELMKMLFNVTYRAAMFEFINMSEMPGLKLSKENTEKGFALTE
IQNLKDTADQALAVRESLVAASNFFTLIPSIHPHIRDEDDLMKAKMLFALQDI
EIASKIVGSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSD
ELEEVFLDRDGLNLYSRKYNLHNNKMLLHWSRUTNFVGLISQSLRTAPPEPVTG
YMFGLYFADLYSKSAOYCYVDNRNPNVGLMLLSEVALGDMYLEKKATSKMDKPPKRGH
STKGLGKTVPLESEFVKWRDDVVVPCPKVPSSIRSELNMEYIYVNTSQVKMQFLL
KVRPHKRR"
```

BASE COUNT 1003 a 617 c 828 g 837 t

ORIGIN

alignment_scores:

Quality: 828.00 Length: 157

Ratio: 5.274 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-236-995D-4 x AF093627

Align seg 1/1 to: AF093627 from: 1 to: 3285

1 AsnLysMetLeuLeuTrpHisGlySerArgLeuThrAsnPheValGlyI 17

2569 AACAAAGATGCTATTATGGCAGCGTTCAAGGTTGACCAATTTGTGGGAAT 2618

17 eLeuSerGlnGlyLeuArgIleAlaProProGluAlaProValThrGlyT 34

2619 TCCTAGTCAGGCGTGAAGATTCACCTCTCTGAGGCACCTGTTACTGGCT 2668

34 yrMetPheGlyLysGlyLeuTyrrPheAlaAspLeuValSerLysSerAla 50

2669 ATATGTTCCGCAAGGCGCTCTACTTTTCAGATCTAGTAAGCAAGCGCA 2718

51 GlnTyrrCysTyrrValAspArgAsnProValGlyLeuMetLeuLeuSe 67

2719 CAATACCTGTTATGTTGGATAGGAATAATCCTGATAGTTGTGCTCTTCTTC 2768

67 rGluValAlaLeuGlyAspMetTyrrGluLeuLysLysAlaThrSerMetA 84

2769 TGAGTTGCTTTAGGACACATGATGAACATAAAGAAAGCCACGTCATGG 2818

84 spLysProProArgGlyLysHisSerThrLysGlyLeuGlyLysThrVal 100

2819 ACAAACTCCCAAGAGGGAAGCATTCGACCAAGGATTAGCAAAACCGTG 2868

101 ProLeuGluSerGluPheValLysTrpArgAspValValValProCy 117

2869 CCATGAGTCAAGATTTGTGAAGTGGAGGATGATGCTGCTAGTTCCTG 2918

117 sGlyLysProValProSerSerIleArgSerSerGluLeuMetTyrrAsnG 134

2919 CGCAAGCGCGTGCATCATCAATAGGAGCTCTGAACACTCATGTACAATG 2968

134 luTyrrIleValTyrrAsnThrSerGlnValLysMetGlnPheLeuLys 150

2969 AGTACATCGTCTACAAACACATCCAGGTGAAGATGCAGTCTTCTGCTGAAG 3018

```
1 AsnLysMetLeuLeuTrpHisGlySerArgLeuThrAsnPheValGlyI 17
|||||
2549 AACAAAGATGCTATTATGGCAGCGTTCAAGGTTGACGAATTTGTGGGAAT 2598
|||||
17 eLeuSerGlnGlyLeuArgIleAlaProProGluAlaProValThrGlyT 34
|||||
2599 TCCTAGTCAGGCGTGAAGATTCACCTCTCTGAGGCACCTGTTACTGGCT 2648
|||||
34 yrMetPheGlyLysGlyLeuTyrrPheAlaAspLeuValSerLysSerAla 50
|||||
2649 ATATGTTCCGCAAGGCGCTCTACTTTTCAGATCTAGTAAGCAAGCGCA 2698
|||||
51 GlnTyrrCysTyrrValAspArgAsnProValGlyLeuMetLeuLeuSe 67
|||||
2699 CAATACCTGTTATGTTGGATAGGAATAATCCTGATAGTTGTGCTCTTCTTC 2748
|||||
67 rGluValAlaLeuGlyAspMetTyrrGluLeuLysLysAlaThrSerMetA 84
|||||
2749 TCAGGTTGCTTTAGGACACATGATGAACATAAAGAAAGCCACGTCATGG 2798
|||||
84 spLysProProArgGlyLysHisSerThrLysGlyLeuGlyLysThrVal 100
|||||
2799 ACAAACTCCCAAGAGGGAAGCATTCGACCAAGGATTAGGCAAAACCGTG 2848
|||||
101 ProLeuGluSerGluPheValLysTrpArgAspValValValProCy 117
|||||
2849 CCATGAGTCAAGATTTGTGAAGTGGAGGATGATGCTGCTAGTTCCTG 2898
|||||
117 sGlyLysProValProSerSerIleArgSerSerGluLeuMetTyrrAsnG 134
|||||
2899 CGCAAGCGCGTGCATCATCAATAGGAGCTCTGAACACTCATGTACAATG 2948
|||||
134 luTyrrIleValTyrrAsnThrSerGlnValLysMetGlnPheLeuLys 150
|||||
2949 AGTACATCGTCTACAAACACATCCAGGTGAAGATGCAGTCTTCTGCTGAAG 2998
|||||
151 ValArgPheHisHisLysArg 157
|||||
2999 GTGCGTTTCCATCACAAAGAGG 3019
|||||
seq_name: gb_pl:AF093627
seq_documentation_block:
LOCUS AF093627 3285 bp mRNA PLN 29-NOV-1998
DEFINITION Zea mays poly(ADP)-ribose polymerase (PARP1) mRNA, complete cds.
ACCESSION AF093627
VERSION AF093627.1 GI:3928870
KEYWORDS Zea mays.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS 1 (bases 1 to 3285)
TITLE Mahajan,P.B. and Zuo,Z.
JOURNAL Purification and cDNA cloning of maize Poly(ADP)-ribose polymerase
MEDLINE Plant Physiol. 118 (3), 895-905 (1998)
99026291
REFERENCE
AUTHORS 2 (bases 1 to 3285)
TITLE Mahajan,P.B. and Zuo,Z.
JOURNAL Direct Submission
TITLE Submitter
JOURNAL Submitted (22-SEP-1998) Crop Protection, Pioneer HiBred
International, Inc., 7300 NW 62nd Avenue, Johnston, IA 50131-1004,
USA
FEATURES
Source
1. 3285
/organism="Zea mays"
/db_xref="taxon:4577"
1. 3285
/gene="PARP1"
100..3042
/gene="PARP1"
/EC_number="2.4.2.30"
```

|||||
2790 GTATGAACCTAAGAAAGCCACGTCCTCCATGACAAACCTCCAAAGGAGGAC 2839
916 isSerThrLysGlyLeuGlyLysThrValProLeuGluSerGluPheVal 932
|||||
2840 ATTGCGACCAAGGATTAGGCAAAACCGTCCACTGGAGTCAGAGTTGTG 2889
933 LysTrpArgAspValValProCysGlyLysProValProSerSe 949
|||||
2890 AAGTGGAGGATGATGTCGTAGTTCCTCGCGCAAGCCGTCATCATC 2939
949 rIleArgSerSerGluLeuMetTyrAsnGluTyrIleValTyrAsnThrS 966
|||||
2940 AATTAGGAGCTCTGAATCATGTACATGAGTACATGCTCTACAACAT 2989
966 erGlnValLysMetGlnPheLeuLysValArgPheHisLysArg 982
|||||
2990 CCCAGGTGAAGATGCACTCTCTGCTGAAGTGGCTTCCATCACAAGAGG 3039

seq_name: gb_pl:ZMPARP2

seq_documentation_block: 3211 bp mRNA PLN 19-NOV-1997
LOCUS ZMPARP2
DEFINITION Zea mays mRNA for poly(ADP-ribose) polymerase (3211bp).

ACCESSION AJ222589
VERSION AJ222589.1 GI:2632128
KEYWORDS PARP gene; poly(ADP-ribose) polymerase.
SOURCE Zea mays.

ORGANISM Zea mays

REFERENCE 1 (bases 1 to 3211)
AUTHORS Babiychuk, E., Cottrell, P., Storozhenko, S., Fuanthong, M., O'Farrell, M., Van Montagu, M., Inze, D. and Kushnir, S.
TITLE Higher plants possess two poly(ADP-ribose) polymerases
JOURNAL Unpublished
AUTHORS Kushnir, S.
REFERENCE 2 (bases 1 to 3211)
TITLE Direct Submission
JOURNAL Submitted (14-NOV-1997) Kushnir S., VTB, Dep. Genetics, Ledegancstraet 35, Gent, B9000, Belgium

FEATURES
1. 3211
/organism="Zea mays"
/db_xref="taxon:4577"
113..3022
/gene="PARP"
113..3022
/gene="PARP"
/function="secondary protein modification"
/product="poly(ADP-ribose) polymerase"
/protein_id="CAA10889.1"
/db_xref="GI:2632128"
/translation="MAAPKAAEYAKSRASCKSCRSPIAKDQELCKMVAOSFD
GMPWNHNSVDDVEGIDALRWDDQEKIRNYGSASAGTSSTAAPPEKCTIEASAR
TSCRCSEKITKGSVRLSAKLESEGPKGIPWYHANCFFVSPSATVEKSGWDTLSDE
DKRMLDLVKDGVNNEONKGRKSKENDIDSYKARLDESEGTVRNKGOLVDR
GNTSSADIQLKLEQSDTLWKDLGKTHVSAELRDLMEANGQDTSGPERHLDR
ADGMIFGALGFCPVCCANGMYNYNGOCNGVSEWSEKCTYSATPEVRVKKWQIPHT
KNDYLMFKSOKVKKPFRVLPWSPKSGSKATQRYSLSSKGLDKLRFSVVGQSK
AANWIEKLAGANFYARVVDIDLACGLDNEAENAEVKKARLKIPIVRGTYGE
CVKKNMLPFDLYKLENALESKGTSTVTVKVSVAHSESGDQTAHILEDGKSYN
ATVNSDLALGVNSYVLIITQDDGSECVYFRKWRVSGSEKIGQKLEEMSEKIAIK
EKKRLFEKTGNSWEAKETNFRKQGRFPLVDYGVKKAKRKDKIEMKSSLAPO
LEELMKMLPNVETYEAMWEFINMSEMPGLKSKENIEKGFALTEIQLNLDADQ
ALAVRESLIVASNRFFLIPSLIHPHIIIRDEDDLMIRAKMLEALQDLEIAKIVGDS
DSELDKDKYMKLHCDITPLAHDSEYKLIIEQYLLNTHAPTHKDWLSLEVEFLDQ
GELNKYSRYKNLHNKMLHGSRLTNFVLISQGLRIAPPEAPVTCYMGKGLYFAD
LVSKSAQCYVDNRNPNVGLMLSEVALGDMYELKATSNDRAPPRKGTSGKGLKTVPL
ESEFVKWRDDVVVPCGKVPSSIRSELINYEIVYNTSQVKMQFLKVRFHHR"

source

gene

CDS

599 rAsnPheArgLysGlnPro
|||||
1893 CAATTTCGGAAGCAGCCT
616 lYValLysLysAlaProLY
|||||
1943 GTGTTAAGAAAGCACCAM
633 LeuAlaProGlnLeuLeu
|||||
1993 CTTGCTCTCAATTGCTA
649 rTyrArgAlaAlaMetMetGluPheGlu***
2043 ATATAGAGCTCTATGATGAATTTGAATTAATATGTCAGAAATGCCTC 2092
666 euGlyLysLeuSer*****AsnIleGlu**GlyPheGluAlaLeuThr 682
|||||
2093 TTGGGAAGCTTAATTTGTTGCTGCGAGCAATCGCTTTTTCACCTCTATCCC 2142
683 *****LeuPheGluGlyHisArg***SerSerThrGlyLeu** 699
|||||
2143 GAGATACAGATTTATT.GAAGACACCGCTGATCAAGCACTGCTG.TT 2190
699 *GluLysAla***LeuLeu*****PheSerLeuLeuSerL 716
|||||
2191 AGAGAAAGCTTAATTTGTTGCTGCGAGCAATCGCTTTTTCACCTCTATCCC 2240
716 euLeuPheIleLeuIleLeuTyrGlyMetArgMetIleSerTyrSerLys 732
|||||
2241 TTTCTATTCTCATATATATACGGGATGAGGATGATTG.ATGATCAA 2289
733 AlaLysMetLeuGluAlaLeuGlnAspIleGluIleAlaSerLysIleVa 749
|||||
2290 GCGAAATGCTTCAAGCTCTGAGGATATTGAATTTGCTTCAAGATAGT 2339
749 lGlyPheAspSerAspSerAspGluSerLeuAspLysTyrMetLysL 766
|||||
2340 TGGCTTCGATAGCAGCAGTGAATCTCTTCTGATGATAAATATGAAC 2389
766 euHisCysAspIleThrProLeuAlaHisAspSerGluAspTyrLysLeu 782
|||||
2390 TTCACGTGACATCACCCCGCTCGCTCAGCATAGTGAAGATTACAAAGTTA 2439
783 lIleGluGlnTyrLeuLeuAsnThrHisAlaProThrHisLysAspTrpSe 799
|||||
2440 ATTGAGCAGTATCTCTCAACACACATAGTCTCTTACTCAAGAGCAGTGC 2489
799 rLeuGluLeuGluGluValPheSerLeuAspArgAspGlyGluLeuAsnL 816
|||||
2490 GCTGGAAGCTGAGGAAGCTTTTTCACCTTGATCGAGATGGAAGCTTAATA 2539
816 ystYrSerArgTyrLysAsnAsnLeuHisAsnLysMetLeuLeuTyrPHis 832
|||||
2540 AGTACTCAAGATATAAATAAATCTGCATACCAAGATGCTATTATGCGAC 2589
833 GlySerArgLeuThrAsnPheValGlyIleLeuSerGlnGlyLeuArgII 849
|||||
2590 GTTCAAGGTTGACGAATTTTGTGGGAATCTTAGTCAAGGGCTAAGAAAT 2639
849 eAlaProProGluAlaProValThrGlyTyrMetPheGlyLysGlyLeuT 866
|||||
2640 TGCACCTCTGAGGCACCTGTTACTGCTATATGTCGCAAGAGGCGCTCT 2689
866 yTPheAlaAspLeuValSerLysSerAlaGlnTyrCysTyrValAspArg 882
|||||
2690 ACTTTGAGATCTAGTAAGCAAGAGCGCCACCAATCTGTTATGATGATAGG 2739
883 AsnAsnProValGlyLeuMetLeuLeuSerGluValAlaLeuGlyAspMe 899
|||||
2740 AATAATCTGCTAGTGTGATGCTCTTCTGAGGTGCTTTAGAGACAT 2789
899 tTyrGluLeuLysLysAlaThrSerMetAspLysProArgGlyLysH 916

Mon Mar 11 09:58:37 2002

BASE COUNT 968 a 604 c 813 g 826 t
ORIGIN

alignment_scores:
Quality: 4666.50 Length: 985
Ratio: 4.980 Gaps: 6
Percent Similarity: 95.127 Percent Identity: 94.416

alignment_block:

US-09-236-995D-2 x ZMPARP2

Align seg 1/1 to: ZMPARP2 from: 1 to: 3211

1 MetAlaLaProProLysAlaThrPlyAlaGluTyrAlaLysSerGlyAr 17
113 ATGGCGGCGCCGCAAGAGCGGTGAAGCGGAGTATGCCAAGTCTGGCG 162
17 gAlaSerCysLysSerCysArgSerProIleAlaLysAspGlnLeuArgL 34
163 GGCCTCGTGCAGTCAATGCCCGTCCCTATGCCAAGSACCAGCTCCGTC 212
34 euGlyLysMetValGlnAlaSerGlnPheAspGlyPheMetProMetTip 50
213 TTGGCAAGATGTTTCCAGCGTCACAGTTTCGACGCTTCATGCCGATGTG 262
51 AsnHisAlaArgCysIlePheSerLysLysAsnGlnIleLysSerValas 67
263 AACCATGCG.....ACGGTTGA 279
67 pAspValGluGlyIleAspAlaLeuArgTyrAspAspGlnGluLysIleA 84
280 CGATGTTGAAGGATAGATGCACCTTAGATGGGATGATCAAGAGAGATAC 329
84 rgAsnTyrValGlySerAlaSerAlaGlyThrSerThrAlaAlaPro 100
330 GAAACTACGTTGGAGTGGCTCAGCTGGGTACAGTTCTACAGCTGCTCT 379
101 ProGluLysCysThrIleGluIleAlaProSerAlaArgThrSerCysAr 117
380 CCGAGAAATGACATTCAGATGCTGCTCCATCTGCCCGTACTTCATGTAG 429
117 gArgCysSerGluLysIleThrLysGlySerValArgLeuSerAlaLysL 134
430 ACGATGCACTGAAAGATTACAAAGGATCGGTCCGCTCTTCAGCTAAGC 479
134 euGluSerGluGlyProLysGlyIleProTyrPyrHisAlaAsnCysPhe 150
480 TTGAGAGTGAAGGTCCCAAGGGTATACCATGGTATCATGCCAATCTTTC 529
151 PheGluValSerProSerAlaThrValGluLysPheSerGlyTrpAspTh 167
530 TTTGAGGTATCCCGTCTGCAACTGTTGAGAAGTTCTCAGCTGGGATAC 579
167 rIeuSerAspGluAspLysArgThrMetLeuAspLeuValLysLysAspV 184
580 TTGTGCCGATGAGGATAGAGAACCACTGCTCGATCTTGTAAAAAGATG 629
184 alGlyAsnAsnGluGlnAsnLysGlySerLysArgLysLysSerGluAsn 200
630 TTGGCAACAANTCAACAAAATAAGGTTCCAGGCCAAGAAAGTGAAT 679
201 AspIleAspSerTyrLysSerAlaArgLeuAspGluSerThrSerGluG 217
680 GATATTGATGCTACAAATCCCGAGGTAGTGAAGTACATCTGAAGG 729
217 yThrValArgAsnLysGlyGlnLeuValAspProArgGlySerAsnThrS 234
730 TACAGTCCGAAACAAAGGCAACTTGTAGACCCACGCTGTTCCCAATACTA 779
234 erSerAlaAspIleGlnLeuLysLysLysGluGlnSerAspThrLeuTip 250
780 GTTCAGCTGATATCCAACTAAAGCTTAAGGAGCAAGTGACACACTTTGG 829

251 LysLeuLysAspGlyLeuLysThrHisValSerAlaAlaGluLeuArgAs 267
830 AAGTTAAAGGATGGACTTAAGACTCATGTATCGGCTGCTGAATTAAGGA 879
267 pMetLeuGluAlaAsnGlyGlnAspThrSerGlyProGluArgHisLeuL 284
880 TATGCTTGAGGCTAATGGCAGCATACATCAGGACCAGAAAGGCACCTAT 929
284 euAspArgCysAlaAspGlyMetLeuPheGlyAlaLeuGlyProCysPro 300
930 TGGATCGCTGTGCGGATGAATTTGGAGCGCTGGTCTCTTGCCCA 979
301 ValCysAlaAsnGlyMetTyrTyrAsnGlyGlnTyrGlnCysSerGl 317
980 GTCTGTGCTAATGGCATGTACTATTATATATGTCAGTACCAATGCGTGG 1029
317 yAsnValSerGluTyrSerLysCysThrTyrSerAlaThrGluProVala 334
1030 TAATGTGTGAGGTGGTCCAAAGTGTACTACTTGCACAGAACCTGTGCC 1079
334 rgValLysLysLysTyrGlnIleProHisGlyThrLysAsnAspTyrLeu 350
1080 GCGTTAAAGAGAGTGGCAAAATTCACATGGAACAAGAATGATTACCTT 1129
351 MetLysTyrPheLysSerGlnLysValLysLysProGluArgValLeuPr 367
1130 ATGAAGTGGTTCAAAATCTCAAAAGGTTAAGAAACACAGAGAGGTTCTTC 1179
367 pProMetSerProGluLysSerGlySerLysAlaThrGlnArgThrSerL 384
1180 ACCAATGTCACTGAGAAATCTGGAAGTAAAGCACTCAGAGAACATCAT 1229
384 euLeuSerSerLysGlyLeuAspLysLeuArgPheSerValValGlyGln 400
1230 TCGCTGCTCTTAAAGGTTGGATRAAATTAAGCTTTTCTGTGTAGGACA 1279
401 SerLysGluAlaAlaAsnGluTyrIleGluLysLysLeuAlaGlyAl 417
1280 TCAAAAGAGACACAAATGCTGGATTGAGAAGCTCAAACTTGTGTGTGC 1329
417 aAsnPheTyrAlaArgValValLysAspIleAspCysLeuIleAlaCysG 434
1330 CAACCTCTATGCCAGGTGTCAAGATATTCATTGTTTAAATTCATGTG 1379
434 lyGluLeuAspAsnGluAsnAlaGluValArgLysAlaArgLeuLys 450
1380 GTGAGCTCGACAATGAAATGCTGAAGTCAGGAAAGCAAGGAGGCTGAAG 1429
451 IleProIleValArgGluGlyTyrIleGlyGluCysValLysArgThrL 467
1430 ATACCAATTGTAAAGGAGGTTTACATTGGAGATGCTGTTAAAGAACAA 1479
467 yCysCysHisLeuIleCysIleAsn..TrpAsnAlaLeuGluSerSerL 483
1480 AATGCTCCATTTGATTGTTATAACTAGAGAATGCTTAGAGTCTCTCAA 1529
483 ysGly***ThrValThrValLysValLysGlyArgSerAlaCysSer*** 499
1530 AAGCAGTACTGTACCTGTTAAAGTTAAGGCCGGAAGTCTGTTTCATGAG 1579
500 SerPro***ValCysLysAsnThrAlaHisIlePro****TrpGluLys 1625
1580 TCCCTGCTGTTG...CAAGATATGCTCACTTCTTGA..AGATGGGAAA 1625
516 shIleGlnCys***LeuLysHisValLeuThr***His***ValCys. 532
1626 GCATATACATGCAACCTTAAACATGCTGACCTGGC...ACTAGGTGTG 1672
533 ThrGlyTyrTyrValLeuGlnIleIleGluGlnAspAspGlySerGluCy 549
1673 AACAGCTACTATGTACTCCATCATTTGACAGGATGATGGTCTGAGTG 1722

549 stYrValPheArgLysTyrGlyArgValGlySerGluLysIleGlyGlyC 566
1723 CTRCGTATTTCTGTAAGTGGGACGGTGGAGTGGAGAAATTTGGAGGCG 1772
566 lYlYsLeuGluGluMetSerLysThrGluAlaIleLysGluPheLysArg 582
1773 AAAAACTGGAGGAGATGTCAAAACTGAGCAATCAAGGAATTCAAAAAG 1822
583 LeuPheLeuGluLysThrGlyAsnSerTyrGluAlaTyrGluCysLysTh 599
1823 TTAATTTCTTGAGACACTGGAACTCATGGAGCTTGGGAATGTAAAC 1872
599 rAsnPheArgLysGlnProGlyArgPheTyrProLeuAspValAspTyrG 616
1873 CAATTTGGAGACGACCTGGGAGATTTTACCCACTTGATGTGATATG 1922
616 lYValLysLysAlaProLysArgLysAspIleSerGluMetLysSerSer 632
1923 GTGTTAAGAAACACCAAAACGGAAGATATACATGAAATGAAAGTTCT 1972
633 LeuAlaProGlnLeuLeuGluMetLysMetLysMetLeuPheAsnValGluTh 649
1973 CTGTCTCTCAATTTCTAGAACTCATGAAGATGCTTTTCAATGTGGAGAC 2022
649 rTyrArgAlaAlaMetMetGluPheGlu***AsnMetSerGluMetProL 666
2023 ATATAGAGCTGCTATGATGGAATTTGAAATTAATATGACAAATGGCTC 2072
666 euGlyLysLeuSer*****AsnIleGlu***GlyPheGluAlaLeuThr 682
2073 TTGGGAGCTAGCAGGAAATATTTGAAAGAGGATTTGAAGCATTAAT 2122
683 *****LeuPheGluGlyHisArg***SerSerThrGlyLeu** 699
2123 GAGATACAGAAATTTATTT.GAAGGACCGCTGATCAAGCACTGGCTG.TT 2170
699 *GluLysAla**LeuLeu*****PheSerLeuLeuSerL 716
2171 AGAGAAAGCTTAATTTGCTCGAGCAATCGCTTTTCACTCTATATCCC 2220
716 euLeuPheIleLeuLeuLeuTyrGlyMetArgMetIleSerTyrSerLys 732
2221 TTCTATTATCTCTCATATTATACGGGATGAGGATGATTTG.ATGATCAAA 2269
733 AlaLysMetLeuGluAlaLeuGlnAspIleGluIleAlaSerLysIleVa 749
2270 GCGAAATCTTGAAGCTCTGACGATATTGAATTTGCTTCAAGATAGT 2319
749 lGlyPheAspSerAspSerAspGluSerLeuAspAspLysTyrMetLysL 766
2320 TGGCTTCGATAGCAGAGTATGAAATCTCTTGTATGATAATATATGAAC 2369
766 euHisCysAspIleThrProLeuAlaHisAspSerGluAspTyrLysLeu 782
2370 TTCACTGTGACATACCCCTGCTGCTCAGCATAGTAGAATTTACAAGTTA 2419
783 lIleGluGlnTyrLeuLeuAsnThrHisAlaProThrHisLysAspTyrSe 799
2420 ATTGAGCAGTATCTCTCAACACACATGCTCTTACTTCAAGAGCTGGTC 2469
799 rLeuGluLeuGluGluValPheSerLeuAspArgAspGlyGluLeuAsnL 816
2470 GCTGGAAGCTGAGGAAGATTTTTCATCTGTATGATGAGAGACTTAATA 2519
816 ystYrSerArgTyrLysAsnAsnLeuHisAsnLysMetLeuLeuTyrPHis 832
2520 AGTACTCAAGATATAAAAAATATCGATACCAAGATGCTATTATGGCAC 2569
833 GlySerArgLeuThrAsnPheValGlyIleLeuSerGlnGlyLeuArgil 849
2570 GGTCAAGGTGAGCAATTTTGGGGAATTTCTTACTCAAGGCTAAGAAAT 866
849 eAlaProProGluAlaProValThrGlyTyrMetPheGlyLysGlyLeuT 866

2620 TGCACCTCTCTGAGCACCTGTTACTGGCTATATGTTGCGCAAAAGCCCTCT 2669
866 yrPheAlaAspLeuValSerLysSerAlaGlnTyrCysTyrValAspArg 882
2670 ACTTTGCAGATCTAGTAAGCAAGAGCGCAATACTTTATGTGTAGTAGG 2719
883 AsnAsnProValGlyLeuMetLeuLeuSerGluValAlaLeuGlyAspMe 899
2720 AATAATCTCTAGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2769
899 tTyrGluLeuLysAlaThrSerMetAspLysProProArgGlyLysH 916
2770 GTATGAACCTAAAGAAAGCCACGTCCTATGGCAAAACCTCCAAGAGGGAAC 2819
916 isSerThrLysGlyLeuGlyLysThrValProLeuGluSerGluPheVal 932
2820 ATTCGACCAAGGGAATAGGCAAAACCGTCCACTGGAGTCAGAGTTTGG 2869
933 LysTyrArgAspValValProCysGlyLysProValProSerSe 949
2870 AAGTGGAGGATGATGCTGTAGTTCTCTGCGCAAGCCGTCATCATC 2919
949 rIleArgSerSerGluLeuMetTyrAsnGluTyrIleValTyrAsnThrS 966
2920 AATTAGGAGCTCTGAACCTATGATGATGATGATGATGATGATGATGATGAT 2969
966 erGlnValLysMetGlnPheLeuLeuLysValArgPheHisLysLysArg 982
2970 CCCAGTGAAGATGCAGTCTCTGCTGAAGTGGCTTTCCATCACAAGAGG 3019
seq_name: gb_pl:ATH131705
seq_documentation_block: 3187 bp mRNA PLN 18-DEC-1998
LOCUS ATH131705 Arabidopsis thaliana mRNA for poly(ADP-ribose) polymerase.
DEFINITION Arabidopsis thaliana mRNA for poly(ADP-ribose) polymerase.
ACCESSION AJ131705
VERSION AJ131705.1 GI:4038490
KEYWORDS NAD(+) ADP-ribosyltransferase; parp-1 gene; poly(ADP-ribose) polymerase.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 3187)
Kazmaier,M.
Direct Submission
Submitted (17-DEC-1998) Kazmaier M., Departement D'Ecophysiologie
Vegetale Et De Microbiologie, Commissariat A L'energie Atomique,
CEA Cadarache, Lab. De Radiobiol. Vegetale, Bat. 185, 13108 St.
paul-les-Durance, FRANCE
2 (bases 1 to 3187)
Doucet-chabeaud,G. and Kazmaier,M.
Unpublished
Location/Qualifiers
1. 3187
/organism="Arabidopsis thaliana"
/cultivar="landsberg erecta"
/db_xref="taxon:3702"
11. 2963
/gene="parp-1"
/gene="parp-1"
/standard_name="NAD(+) ADP-ribosyltransferase"
/EC_number="2.4.2.30"
/function="ADP-Ribose polymer synthesis"
/note="mol. weight: 111 kDa"
/codon_start=1
/evidence=experimental
/product="poly(ADP-ribose) polymerase"
/protein_id="CAA10482.1"
/db_xref="GI:4038491"